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## RAW SEQUENCE LISTING

DATE: 04/23/2002

PATENT APPLICATION: US/10/077,698

TIME: 11:02:07

Input Set : N:\Cr3\RULE60\10077698.raw

Output Set: N:\CRF3\04232002\J077698.raw

1 <110> APPLICANT: Glucksmann, Maria A.  
 2 <120> TITLE OF INVENTION: 14273 Receptor, A Novel G-Protein Coupled Receptor  
 3 <130> FILE REFERENCE: 5800-4B, 035800/177086  
 4 <140> CURRENT APPLICATION NUMBER: 10/077,698  
 5 <141> CURRENT FILING DATE: 2002-02-13  
 6 <150> PRIOR APPLICATION NUMBER: 09/261,599  
 7 <151> PRIOR FILING DATE: 1999-02-26  
 10 <150> PRIOR APPLICATION NUMBER: 09/107,761  
 11 <151> PRIOR FILING DATE: 1998-06-30  
 12 <150> PRIOR APPLICATION NUMBER: 09/223,538  
 13 <151> PRIOR FILING DATE: 1998-12-30  
 14 <160> NUMBER OF SEQ ID NOS: 7  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 361  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Homo sapiens  
 21 <400> SEQUENCE: 1  
 22 Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser  
 23 1 5 10 15  
 24 Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys  
 25 20 25 30  
 26 Gly Asp His Arg Leu Val Leu Ala Val Glu Thr Thr Val Leu Val  
 27 35 40 45  
 28 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu  
 29 50 55 60  
 30 Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn  
 31 65 70 75 80  
 32 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu  
 33 85 90 95  
 34 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His  
 35 100 105 110  
 36 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr  
 37 115 120 125  
 38 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln  
 39 130 135 140  
 40 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala  
 41 145 150 155 160  
 42 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe  
 43 165 170 175  
 44 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser  
 45 180 185 190  
 46 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp

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48    Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
49          210          215          220
50    Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
51    225          230          235          240
52    Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
53          245          250          255
54    Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
55          260          265          270
56    Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
57          275          280          285
58    Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
59    290          295          300
60    Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
61    305          310          315          320
62    Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
63          325          330          335
64    Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
65          340          345          350
66    Arg Asn Asp Leu Ser Ile Ile Ser Gly
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70 <211> LENGTH: 1743
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
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75    gcgggcagcg ggcgacgcgc ccttgccgag cctggagcaa gccaacgcga cccgctttcc 120
76    cttctttctcc gacgtcaagg gcgaccaccg gctggtgctg gccgcggtgg agacaaccgt 180
77    gctggtgctc atctttgcag tgcgtgctgt gggcaacgtg tgccgcttgg tgctggtggc 240
78    gcgcgcagca gcgcgcggcg cgactgcctg cctggctactc aacctcttct gcgcggacct 300
79    gctcttcate agcgtatcc cttctggtgt ggccgtgcgc tggactgagg cctggctgct 360
80    gggcccccgtt gccctgccacc tgcctttcta cgtgatgacc ctgagcggca gcgtcaccat 420
81    cctcacgctg gccgcgggtca gccctggagcg catggtgtgc atcgtgcacc tgcagcgcgg 480
82    cgtgcgggggt cctgggcgggc gggcgcgggc agtgcgtgtg gcgctcatct ggggctattc 540
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84    cgccgaccag gaaatttcga tttgcacact gatttgccc accattcctg gagagatctc 660
85    gtgggatgtc tcttttggtt ctttgaactt cttggtgcca ggactggtca ttgtgatcag 720
86    ttactccaaa attttacaga tcacaaaggc atcaagggaag aggtcacgg taagcctggc 780
87    ctactcggag agccaccaga tccgcgtgtc ccagcaggac ttccggtctt tccgcacct 840
88    ctctctctct atggtctcct tcttcatcat gtggagcccc atcatcatca ccctctctct 900
89    catcctgate cagaacttca agcaagacct ggtcatcttg ccgtccctct tcttctgggt 960
90    ggtggccttc acatttgcta attcagccct aaaccccatc ctctacaaca tgacactgtg 1020
91    caggaatgag tggaagaaaa ttttttgcgt cttctggttc ccagaaaagg gagccatttt 1080
92    aacagacaca tctgtcaaaa gaaatgactt gtcgattatt tctggctaatt tttcttttat 1140
93    agccgagttt ctacacctg gcgagctgtg gcatgctttt aaacagagtt catttccagt 1200
94    accctccate agtgaccctt gctttaagaa aatgaacctt tgcaaataga catccacagc 1260
95    gtcggtaaat taaggggtga tcaccaagtt tcataatatt ttccctttat aaaaggattt 1320
96    gttggccagg tgcagtgtt catgcctgta atcccagcag tttgggaggc tgagggtgggt 1380

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Input Set : N:\Crf3\RULE60\10077698.raw

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97      ggatcacctg aggtcaggag ttcgagacca acctgaccaa catggtgaga cccccgtctc 1440
98      tactaaaaat aaaaaaaaaa attagctggg agtgggtggtg ggcacctgta atcctagcta 1500
99      ctctgggaggc tgaaccagga gaatctcttg aacctgggag gcagagggtg cagtgaagccg 1560
100     agatcgtgcc attgcactcc aaccagggca acaagagtga aactccatct taaaaaaaaa 1620
101     aaaaaaaaga tttgttatgg gttcctttta aatgtgaact tttttagtgt gtttgaata 1680
102     tgatcaaatt taataaatat ttatttatga ctgttcagca aaaaaaaaaa aaaaaaaggg 1740
103     cgg 1743
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 259
107 <212> TYPE: PRT
108 <213> ORGANISM: Unknown
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Unknown Organism: Seven
111     Transmembrane Segment Rhodopsin Superfamily
112 <400> SEQUENCE: 3
113     Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
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115     Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
116         20             25             30
117     Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
118         35             40             45
119     Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
120         50             55             60
121     Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Thr Ala Ile
122         65             70             75             80
123     Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
124         85             90             95
125     Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
126         100            105            110
127     Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
128         115            120            125
129     Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130         130            135            140
131     Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
132         145            150            155            160
133     Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
134         165            170            175
135     Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
136         180            185            190
137     Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys
138         195            200            205
139     Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
140         210            215            220
141     Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
142         225            230            235            240
143     Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
144         245            250            255
145     Ile Ile Tyr
147 <210> SEQ ID NO: 4

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Output Set: N:\CRF3\04232002\J077698.raw

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148 <211> LENGTH: 361
149 <212> TYPE: PRT
150 <213> ORGANISM: Murine ortholog
151 <400> SEQUENCE: 4
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154 Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
155      20                      25                      30
156 Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
157      35                      40                      45
158 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
159      50                      55                      60
160 Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn
161      65                      70                      75                      80
162 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
163      85                      90                      95
164 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
165      100                     105                     110
166 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
167      115                     120                     125
168 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
169      130                     135                     140
170 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
171      145                     150                     155                     160
172 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu
173      165                     170                     175
174 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
175      180                     185                     190
176 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
177      195                     200                     205
178 Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
179      210                     215                     220
180 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
181      225                     230                     235                     240
182 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
183      245                     250                     255
184 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
185      260                     265                     270
186 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
187      275                     280                     285
188 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
189      290                     295                     300
190 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
191      305                     310                     315                     320
192 Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
193      325                     330                     335
194 Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
195      340                     345                     350
196 Arg Asn Asp Leu Ser Val Ile Ser Ser

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Input Set : N:\Crif3\RULE60\10077698.raw

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197          355          360
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200 <211> LENGTH: 1560
201 <212> TYPE: DNA
202 <213> ORGANISM: Murine ortholog
203 <400> SEQUENCE: 5
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205      ttcacacccat cagtgaccac tccagacttg tccggcttta cccgaatctt cacagcggag 120
206      tcgatgaccc tcttgacagc cagagcgcg cgcagctccg ccattctccc ggacgcgtgg 180
207      gccggggccc cggcatgtcc cctgagtgtg cacagacgac gggccctggt cctcgcaca 240
208      ccctggacca agtcaatcgc acccacttcc ctttcttctc ggatgtcaag ggcgaccacc 300
209      ggttggtggt gagcgctcgt gagaccacg ttctgggact catctttgtc gtctcactgc 360
210      tgggcaacgt gtgtgctcta gtgtgggtgg cgcgccgtcg gcgccgtggg gcgtcagcca 420
211      gcttggtgct caacctcttc tgccggtgatt tgctcttcac cagcgccatc cctctagtgc 480
212      tcgtcgtgcg ctggactgag ccctggctgt tggggcccgt cgtctgccac ctgctcttct 540
213      acgtgatgac aatgagcggc agcgtcacga tctcacact ggccgcggtc agcctggagc 600
214      gcattggtgt catcgtgcgc ctccggcgcg gcttgagcgg cccggggcgg cggactcagg 660
215      cggcactgct ggctttcata tggggttact cggcgtcgc cgcgtgccc ctctacatct 720
216      tgttccgcgt ggtccgcgag cgccttcccg gcggggacca ggaaattccg atttgacat 780
217      tggattggcc caaccgcata ggagaaatct catgggatgt gttttttgag actttgaact 840
218      tcttggtgcc gggactggtc attgtgatca gttactccaa aattttacag atcacgaaag 900
219      catcgcggaa gaggttacg ctgagcttgg catactctga gagccaccag atccgagtgt 960
220      cccaacaaga ctaccgactc ttccgcacgc tcttccgtct catggtttcc ttcttcacat 1020
221      tgtggagtcc catcatcatc accatccctc tcatcttgat ccaaaacttc cggcaggacc 1080
222      tggtcactct gccatccctt ttcttctggg tggtgccctt cacgtttgcc aactctgccc 1140
223      taaaccccat actgtacaac atgtcgtctg tcaggaacga atggaggaag attttttgc 1200
224      gcttcttttt tccagagaag ggagccattt ttacagatac gtctgtcagg tgcaatgtaa 1260
225      tgtctgttat ttccagctaa ctagcctctg gtgccaggtg aaccacggtg tgcattgtaa 1320
226      gggagttaac ttcaaggaaa gccaccagt gcgccgtgct ttaaaaatac ccgacttcca 1380
227      acagcagga tctacggagc cagcaaatta aggaatgatc gctcagtata aaaatatttt 1440
228      tccttaaaag aactttctat gggttccttt tgtgaacttt ttttaagtgt tttgtaatat 1500
229      gatctagtta ataaattttt atttataacg tgttcctaca aaaaaaaaaa aaaaaaaaaa 1560
231 <210> SEQ ID NO: 6
232 <211> LENGTH: 300
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <223> OTHER INFORMATION: mature polypeptide of 14273
237 <400> SEQUENCE: 6
238      Leu Val Leu Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu
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240      Val Leu Asn Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro
241          20          25          30
242      Leu Val Leu Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val
243          35          40          45
244      Ala Cys His Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr
245          50          55          60
246      Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val
247          65          70          75          80

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/077,698

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